

Complete Genome Sequence of Porcine Circovirus 2d Strain GDYX

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Porcine circovirus type 2 (PCV2) is the etiologic agent of porcine circovirus-associated disease, and it is mainly divided into five genotypes. Here, we report the complete genome sequence of PCV2 strain GDYX, which belongs to PCV2d and has a unique amino acid variation at position 169 (S to G).

Porcine circovirus type 2 (PCV2) is the causative agent of postweaning multisystemic wasting syndrome (PMWS) (2, 6). This disease was first confirmed in North America in 1997 (4), and subsequently it has been reported in many areas where there is a swine industry, including Europe, South America, Asia, and Australia (1, 3, 12, 15, 17). In recent years, PMWS has become a serious economic problem for the pig-raising industry in China (7, 16).

Porcine circovirus (PCV) belongs to the *Circovirus* genus of the *Circoviridae* family (5, 9). The PCV2 genome is a circular single-stranded DNA with a size of 1,766 to 1,768 nucleotides (10) and contains three major open reading frames (ORF). ORF1 encodes the replicase proteins Rep, which is involved in virus replication, ORF2, which encodes the viral capsid (cap) protein, and ORF3, which encodes a protein that is involved in PCV2-induced apoptosis *in vitro* (8). Previous investigations showed that there were five PCV2 genotypes, including PCV2a, PCV2b, PCV2c, PCV2d, and PCV2e, according to the unified nomenclature outlined by the EU consortium on PCV2 (7, 11, 16). Here, we report the complete genomic sequence of a novel PCV2d strain, GDYX, which is characterized by a unique variation in position 169 (S to G).

GDYX was isolated from tissue samples from pigs with PMWS. The full-length genome of the isolated strain was amplified by using the primers described by Wang and colleagues (16). The PCR products were purified and cloned into a pMD18-T vector (TaKaRa, Japan) and sequenced three times with an automated genome sequencer (Genetic Analyzer 3730XL; Applied Biosystems). The terminal sequences were acquired by using a kit for rapid amplification of cDNA ends (RACE; Clontech, Japan). Sequence alignment was performed using Clustal X 2.1 (14). Phylogenetic trees were constructed using MEGA 4 (13). The complete genomic sequence of GDYX was determined to be 1,767 nucleotides in length, with a GC content of 48.28%. It consists of at least three ORFs, encoding 2 major proteins, the Rep and cap proteins. The genome sequence of GDYX shares 94.7 to 99.7% identity with other Chinese PCV2 strains. Phylogenetic analysis revealed that GDYX belongs to genotype 2d. Previous reports had demonstrated that all genotype PCV2d strains encoded 234 amino acids in the cap protein, and genotype PCV2d was characterized by an insertion in the last codon of the cap gene, a 3-amino-acid mutation in positions 89 (I/R to L), 90 (S to T), and 169 (S to R) (16). Noticeably, a mutation at position 505 (A to G) was observed in the cap protein of GDYX, resulting in an amino acid variation (S to G) at position 169. The relationship between the

genomic variations and changes in the antigenicity and virulence of the isolate need to be further investigated.

Nucleotide sequence accession number. The genome sequence of PCV2 strain GDYX has been deposited in GenBank under the accession number [JX519293](https://www.ncbi.nlm.nih.gov/nuclot/JX519293).

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